



## SEQUENCE LISTING

1

<110> Callen, Walter  
Richardson, Toby  
Frey, Gerhard  
Miller, Carl  
Kazaoka, Martin  
Short, Jay  
Mathur, Eric

<120> ENZYME HAVING ALPHA AMYLASE ACTIVITY  
AND METHODS OF USE THEREOF

<130> 09010-107001

<140> 10/081,739

<141> 2002-02-21

<150> 60/270,495

<151> 2001-02-21

<150> 60/270,496

<151> 2001-02-21

<150> 60/291,122

<151> 2001-05-14

<160> 69

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1311

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated

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gccggaaatct	ccgcaatatg	gattcccccg	gcgagcaagg	gcatgggcgg	cgcctattcg	180
atgggctacg	acccctacga	cttctttgac	ctcggtgagt	acgaccagaa	ggaaacggta	240
gagacgcgct	ttggctccaa	gcaggagctc	gtgaacatga	taaacaccgc	ccacgcctat	300
ggcatgaagg	taatagccga	tatagtcatac	aaccaccgcg	ccggcgggtga	cctggagtgg	360
aacccttcg	tgaacgacta	tacctggacc	gacttctcaa	aggtcgcgctc	gggtaaatac	420
acggccaact	acctcgactt	ccacccgaac	gagctccatg	cgggcgattc	cggaacattt	480
ggaggctatc	ccgacatatg	ccacgacaag	agctggacc	agtaactggct	ctgggccagc	540
caggagagct	acgcggcata	tctcaggagc	atcggcatacg	atgcctggcg	cttcgactac	600
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gttggagagt	actgggacac	caacgtcgac	gctgttctca	actgggcata	ctcgagcggt	720
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aaqqccqtaa	cctttqtaqc	aaaccacqac	accqatataa	tctqqaacaa	qtatccaqcc	900
tacgcgttca	tcctcaccta	cgagggccag	ccgacaatat	tctaccgcga	ctacgaggag	960

tggctcaaca aggataagct caagaacctc atctggatac atgagaacct cgccggagga	1020
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gacaagccgg ggcttataac ctacatcaac ctaggtcga gcaaggccgg aaggtgggtt	1140
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gttagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct	1260
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<211> 436  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetically engineered

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Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile	
35 40 45	
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp	
50 55 60	
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val	
65 70 75 80	
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr	
85 90 95	
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His	
100 105 110	
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr	
115 120 125	
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr	
130 135 140	
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe	
145 150 155 160	
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp	
165 170 175	
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly	
180 185 190	
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val	
195 200 205	
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr	
210 215 220	
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly	
225 230 235 240	
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe	
245 250 255	
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln	
260 265 270	
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn	
275 280 285	
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile	
290 295 300	
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu	
305 310 315 320	
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Glu Asn	

325	330	335	
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu			
340	345	350	
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr			
355	360	365	
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys			
370	375	380	
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp			
385	390	395	400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro			
405	410	415	
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr			
420	425	430	
Cys Gly Val Gly			
435			

&lt;210&gt; 3

&lt;211&gt; 1419

&lt;212&gt; DNA

&lt;213&gt; Environmental

&lt;400&gt; 3

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aaggctgccc caccgttaa cgccaccatg atgcagtatt ttgaatggta ctgcggat	120
gatggcacgt tatggaccaa agtgccaaat gaagccaaca acttatccag ccttggcatc	180
accgctctt ggctgcgccc cgcttacaaa ggaacaagcc gcagcgacgt agggtacgga	240
gtatacact tggatgacct cgccgaattt aatcaaaaag ggaccgtccg cacaataac	300
ggaacaaaag ctcaatatct tcaagccatt caagccccc acgcccgtgg aatgcaagtg	360
tacggcgatg tcgtgttcga ccataaaggc ggcgctgacg gcacgaaatg ggtggacgcc	420
gtcgaagtca atccgtccga ccgcaaccaa gaaatctgg gcacctatca aatccaagca	480
tggacgaaat ttgattttcc cggcgcccc aacacctact ccagctttaa gtggcgctgg	540
taccattttgc acggcggttga ttggacgaa agccggaaaat tgagccgcat ttacaaattc	600
cggcgcatcg gcaaagctg ggattggaa gtagacacgg aaaacggaaa ctatgactac	660
ttaatgtatg ccgacatttga tatggatcat cccgaagtgc tgaccgagct gaaaaactgg	720
ggggaaatggt atgtcaacac aacgaacatt gatgggttcc ggcttgcgtgc cgtcaagcat	780
attaagttca gttttttcc tgattggttg tcgtatgtc gttctcgac tggcaagccg	840
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aaaacagacg gaacgatgtc ttgtttgtat gccccgttac acaacaaatt ttataccgt	960
tccaaatcag gggcgccatt tgatatgcgc acgtaatga ccaataactct catgaaagat	1020
caaccgcacat tggccgtcac ctcgttgcatt aatcatgaca ccgaacccgg ccaagcgctg	1080
cagtcatggg tcgaccatg gtcacaaaccg ttggcttacg cctttattct aactcgccag	1140
gaaggatacc cgtgcgtctt ttatggtgac tattatggca ttccacaata taacattcct	1200
tcgctgaaaa gcaaaatcga tccgctccctc atcgccgcga gggattatgc ttacggaaacg	1260
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aaaccaggat ccggcgccgc cgcaactgatc accgatgggc cgggaggaag caaatggatg	1380
tactgttggc aaacaacacg ctggaaaagt gttctatga	1419

&lt;210&gt; 4

&lt;211&gt; 1539

&lt;212&gt; DNA

&lt;213&gt; Environmental

&lt;400&gt; 4

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ttgctgcctc attctgcacg acggcgccga aatcttaatg ggacgctgat gcagtattt	120
gaatggataca tgcccaatga cgcccaacat tggaagcgct tgcaaaacgca ctcggcatat	180
ttggctgaac acggattttac tgccgtctgg attccccgg catataaggg aacgagccaa	240

gcggatgtgg	gctacggtgc	ttacgacctt	tatgatttag	gggagttca	tcaaaaaggg	300
acggttcga	caaagtacgg	cacaaaaagga	gagctgcaat	ctgcgatcaa	aagtcttcat	360
tcccgcaca	ttaacgttta	cggggatgtg	gtcatcaacc	acaaaggcg	cgctgatgcg	420
accgaagatg	taaccgcgg	tgaagtcgt	cccgctgacc	gcaaccgcgt	aatttcagga	480
gaacaccgaa	ttaaaggctg	gacacattt	catttccgg	ggcgcggcag	cacatacagc	540
gattttaaat	ggcatttgta	ccatTTTgac	ggaaccgatt	gggacgagtc	cgaaagctg	600
aaccgcatct	ataagttca	agaaaaggct	tgggattggg	aagtttccaa	tgaaaacggc	660
aactatgatt	atttgatgt	tgccgacatc	gattatgacc	atcctgtatgt	cgcagcagaa	720
attaagagat	ggggcactt	gtatgccaat	gaactgcaat	tggacggtt	ccgtcttgat	780
gctgtcaaac	acattaaatt	ttctttttt	cgggattggg	ttaatcatgt	caggaaaaaa	840
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aactatttga	acaaaacaaa	tttaatcat	tcagtttt	acgtgccgt	tcattatcat	960
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gtcgTTTca	agcatccgtt	gaaagcgggt	acatttgcg	ataaccatga	tacacagccg	1080
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gactcccagc	gcgaaattcc	tgccTTgaaa	cacaaaattt	aaccgatctt	aaaagcgaga	1260
aaacagtatg	cgtacggagc	acagcatgt	tatttcgacc	accatgacat	tgtcggtgg	1320
acaagggaaag	gcgacagctc	ggttgc当地	tcaggttt	cggttgc当地	aacagacgg	1380
ccccgggggg	caaagcgaat	gtatgtcggc	cgccaaaacg	ccgggtgagac	atggcatgac	1440
attaccggaa	accgttcgga	gccggTTgtc	atcaatttgcg	aaggctgggg	agagtttac	1500
gttaaacggcg	ggtcggTTt	aatttatgtt	caaagatag			1539

&lt;210&gt; 5

&lt;211&gt; 1395

&lt;212&gt; DNA

&lt;213&gt; Environmental

&lt;400&gt; 5

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ctactctcga	ctccagtggg	tgctgccaag	tactccgaac	tcgaagagg	cggtgttata	120
atgcaggcct	tctactggg	tgttcccgg	ggggaaatct	ggtgggacac	cataagacag	180
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tactatcaga	agggAACAGT	tgagacgcgc	ttcggtcaa	aggaggaact	ggtaacatg	360
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gccgggtggag	accttgatgt	gaacccttt	gtaaacaact	atacttggac	agacttctcc	480
aaggtcgcc	ccggtaata	cacggccaac	taccttgact	tccacccaa	cgaggtaag	540
tgctgcgt	agggtacatt	tgttgactt	ccggacatcg	cccacgagaa	gagctggat	600
cagtactggc	tctggcaag	caatgagagc	tacgccc	atctccggag	catagggatc	660
gatgcattggc	gtttcgact	cgtaaagg	tacggagcg	gggtttaa	tgactggctc	720
agctgggtgg	gaggctggc	cgttggagag	tactggaca	cgaacgttga	tgcactcctt	780
aactgggcatt	acgacagcgg	tgccaagg	tttgacttcc	cgctctacta	caagatggac	840
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cacgagcacc	ttggccggagg	aagtaccaag	atccttact	acgataacg	tgagctaata	1140
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tacacaggca	atctcggt	ctgggttgc	agggtgg	atgtacgtgg	atgggttaaa	1320
ctgacggcac	ctcctcatg	tccagccaa	ggatattacg	gctactcgt	ctggagctac	1380
gcaggcgtcg	gatga					1395

&lt;210&gt; 6

&lt;211&gt; 1386

&lt;212&gt; DNA

## &lt;213&gt; Bacteria

&lt;400&gt; 6

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gccttctact	gggacgtccc	aggtggagga	atctgggg	acaccatca	gagcaagata	180
ccggagtgg	acgaggccgg	aatatccgc	atttggattc	cgcgcaggcc	caagggatg	240
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gggtga						1386

&lt;210&gt; 7

&lt;211&gt; 472

&lt;212&gt; PRT

&lt;213&gt; Environmental

&lt;400&gt; 7

Met	Phe	Leu	Leu	Ala	Phe	Leu	Leu	Thr	Ala	Ser	Leu	Phe	Cys	Pro	Thr
1					5				10				15		
Gly	Gln	Pro	Ala	Lys	Ala	Ala	Ala	Pro	Phe	Asn	Gly	Thr	Met	Met	Gln
									20			25			30
Tyr	Phe	Glu	Trp	Tyr	Leu	Pro	Asp	Asp	Gly	Thr	Leu	Trp	Thr	Lys	Val
									35			40			45
Ala	Asn	Glu	Ala	Asn	Asn	Leu	Ser	Ser	Leu	Gly	Ile	Thr	Ala	Leu	Trp
									50			55			60
Leu	Pro	Pro	Ala	Tyr	Lys	Gly	Thr	Ser	Arg	Ser	Asp	Val	Gly	Tyr	Gly
									65			70			75
Val	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val
									85			90			95
Arg	Thr	Lys	Tyr	Thr	Lys	Ala	Gln	Tyr	Leu	Gln	Ala	Ile	Gln	Ala	
									100			105			110
Ala	His	Ala	Ala	Gly	Met	Gln	Val	Tyr	Ala	Asp	Val	Val	Phe	Asp	His
									115			120			125
Lys	Gly	Gly	Ala	Asp	Gly	Thr	Glu	Trp	Val	Asp	Ala	Val	Glu	Val	Asn
									130			135			140
Pro	Ser	Asp	Arg	Asn	Gln	Glu	Ile	Ser	Gly	Thr	Tyr	Gln	Ile	Gln	Ala
									145			150			155
Trp	Thr	Lys	Phe	Asp	Phe	Pro	Gly	Arg	Gly	Asn	Thr	Tyr	Ser	Ser	Phe
									165			170			175
Lys	Trp	Arg	Trp	Tyr	His	Phe	Asp	Gly	Val	Asp	Trp	Asp	Glu	Ser	Arg

180	185	190
Lys Leu Ser Arg Ile Tyr Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp		
195	200	205
Trp Glu Val Asp Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala		
210	215	220
Asp Leu Asp Met Asp His Pro Glu Val Val Thr Glu Leu Lys Asn Trp		
225	230	235
Gly Lys Trp Tyr Val Asn Thr Asn Ile Asp Gly Phe Arg Leu Asp		
245	250	255
Ala Val Lys His Ile Lys Phe Ser Phe Pro Asp Trp Leu Ser Tyr		
260	265	270
Val Arg Ser Gln Thr Gly Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp		
275	280	285
Ser Tyr Asp Ile Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asp Gly		
290	295	300
Thr Met Ser Leu Phe Asp Ala Pro Leu His Asn Lys Phe Tyr Thr Ala		
305	310	315
Ser Lys Ser Gly Gly Ala Phe Asp Met Arg Thr Leu Met Thr Asn Thr		
325	330	335
Leu Met Lys Asp Gln Pro Thr Leu Ala Val Thr Phe Val Asp Asn His		
340	345	350
Asp Thr Glu Pro Gly Gln Ala Leu Gln Ser Trp Val Asp Pro Trp Phe		
355	360	365
Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro		
370	375	380
Cys Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro		
385	390	395
Ser Leu Lys Ser Lys Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr		
405	410	415
Ala Tyr Gly Thr Gln His Asp Tyr Leu Asp His Ser Asp Ile Ile Gly		
420	425	430
Trp Thr Arg Glu Gly Val Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala		
435	440	445
Leu Ile Thr Asp Gly Pro Gly Ser Lys Trp Met Tyr Cys Trp Gln		
450	455	460
Thr Thr Arg Trp Lys Ser Val Leu		
465	470	

<210> 8

<211> 512

<212> PRT

<213> Environmental

<400> 8

Met Lys Gln Gln Lys Arg Leu Tyr Ala Arg Leu Leu Thr Leu Leu Phe			
1	5	10	15
Ala Leu Ile Phe Leu Leu Pro His Ser Ala Ala Ala Ala Asn Leu			
20	25	30	
Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro Asn Asp Gly			
35	40	45	
Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu Ala Glu His			
50	55	60	
Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln			
65	70	75	80
Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe			
85	90	95	
His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu Leu			

100	105	110
Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr Gly		
115	120	125
Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp Val		
130	135	140
Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser Gly		
145	150	155
Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg Gly		
165	170	175
Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Thr		
180	185	190
Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln Gly		
195	200	205
Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp Tyr		
210	215	220
Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala Glu		
225	230	235
Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp Gly		
245	250	255
Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg Asp		
260	265	270
Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr Val		
275	280	285
Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu Asn		
290	295	300
Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr Gln		
305	310	315
Phe His Ala Ala Ser Thr Gln Gly Gly Tyr Asp Met Arg Lys Leu		
325	330	335
Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr Phe		
340	345	350
Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr Val		
355	360	365
Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Glu		
370	375	380
Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys Gly		
385	390	395
Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro Ile		
405	410	415
Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr Phe		
420	425	430
Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser Val		
435	440	445
Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ala		
450	455	460
Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His Asp		
465	470	475
Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly Trp		
485	490	495
Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln Arg		
500	505	510

<210> 9  
<211> 464  
<212> PRT  
<213> Environmental

&lt;400&gt; 9

Val Val His Met Lys Leu Lys Tyr Leu Ala Leu Val Leu Leu Ala Val  
 1 5 10 15  
 Ala Ser Ile Gly Leu Leu Ser Thr Pro Val Gly Ala Ala Lys Tyr Ser  
 20 25 30  
 Glu Leu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val  
 35 40 45  
 Pro Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln Lys Ile Pro Glu  
 50 55 60  
 Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys  
 65 70 75 80  
 Gly Met Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe  
 85 90 95  
 Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe Gly  
 100 105 110  
 Ser Lys Glu Glu Leu Val Asn Met Ile Asn Thr Ala His Ser Tyr Gly  
 115 120 125  
 Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp  
 130 135 140  
 Leu Glu Trp Asn Pro Phe Val Asn Asn Tyr Thr Trp Thr Asp Phe Ser  
 145 150 155 160  
 Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro  
 165 170 175  
 Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Asp Phe Pro Asp  
 180 185 190  
 Ile Ala His Glu Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser Asn  
 195 200 205  
 Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile Asp Ala Trp Arg  
 210 215 220  
 Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Asn Asp Trp Leu  
 225 230 235 240  
 Ser Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val  
 245 250 255  
 Asp Ala Leu Leu Asn Trp Ala Tyr Asp Ser Gly Ala Lys Val Phe Asp  
 260 265 270  
 Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Thr Asn Ile  
 275 280 285  
 Pro Ala Leu Val Tyr Ala Leu Gln Asn Gly Gly Thr Val Val Ser Arg  
 290 295 300  
 Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile  
 305 310 315 320  
 Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly  
 325 330 335  
 Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp  
 340 345 350  
 Lys Leu Asn Asn Leu Ile Trp Ile His Glu His Leu Ala Gly Gly Ser  
 355 360 365  
 Thr Lys Ile Leu Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Met Arg Glu  
 370 375 380  
 Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Asn  
 385 390 395 400  
 Asp Trp Ala Glu Arg Trp Val Asn Val Gly Ser Lys Phe Ala Gly Tyr  
 405 410 415  
 Thr Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Arg Trp  
 420 425 430  
 Val Gln Tyr Asp Gly Trp Val Lys Leu Thr Ala Pro Pro His Asp Pro  
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Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr Ala Gly Val Gly  
 450                          455                          460

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<212> PRT  
<213> Bacteria

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 1                        5                        10                        15  
Met Ala Val Val Ala Gln Pro Ala Ser Ala Ala Lys Tyr Ser Glu Leu  
 20                      25                      30  
Glu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Gly  
 35                      40                      45  
Gly Gly Ile Trp Trp Asp Thr Ile Arg Ser Lys Ile Pro Glu Trp Tyr  
 50                      55                      60  
Glu Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met  
 65                      70                      75                      80  
Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu  
 85                      90                      95  
Gly Glu Tyr Asn Gln Lys Gly Thr Ile Glu Thr Arg Phe Gly Ser Lys  
 100                     105                     110  
Gln Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys  
 115                     120                     125  
Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Asp Leu Glu  
 130                     135                     140  
Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val  
 145                     150                     155                     160  
Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu  
 165                     170                     175  
Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala  
 180                     185                     190  
His Glu Lys Ser Trp Asp Gln His Trp Leu Trp Ala Ser Asp Glu Ser  
 195                     200                     205  
Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp  
 210                     215                     220  
Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asn Trp  
 225                     230                     235                     240  
Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala  
 245                     250                     255  
Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe Asp Phe Pro  
 260                     265                     270  
Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Lys Asn Ile Pro Ala  
 275                     280                     285  
Leu Val Ser Ala Leu Gln Asn Gly Gln Thr Val Val Ser Arg Asp Pro  
 290                     295                     300  
Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp  
 305                     310                     315                     320  
Asn Lys Tyr Leu Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro  
 325                     330                     335  
Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu  
 340                     345                     350  
Asn Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Ser  
 355                     360                     365  
Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile Phe Val Arg Asn Gly Tyr  
 370                     375                     380

Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys  
 385                   390                   395                   400  
 Val Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His  
                  405                   410                   415  
 Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Tyr Val Tyr Ser  
                  420                   425                   430  
 Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala Tyr Asp Pro Ala Asn Gly  
                  435                   440                   445  
 Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly  
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<220>  
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<400> 11  
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<210> 12  
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<400> 12  
gaacggtctc attccgccag ccagcaaggg gatgagcgg                   39

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<400> 13  
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<210> 14  
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<400> 14  
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<210> 15  
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gaaccgtctc acgatataat ctggaacaag tacttgc		38
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gaaccgtctc aaaggtgggt ttatgtgccg		30
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<220>  
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<400> 20  
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<400> 21  
gaacggtctc agtttatcat attgatgagc tcc 33

<210> 22  
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<220>  
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<400> 22  
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<210> 23  
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<400> 23  
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<400> 24  
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<210> 26  
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<400> 26  
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<220>  
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<400> 42  
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<210> 43  
<211> 33  
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<220>  
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<400> 43  
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<210> 44  
<211> 34  
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<220>  
<223> Primer

<400> 44  
gaaccgtctc acttccaccg gcgagggtgg cgtg 34

<210> 45  
<211> 32  
<212> DNA  
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<220>  
<223> Primer

<400> 45  
gaaccgtctc accttccggc ctggctcgag cc 32

<210> 46  
<211> 35  
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<220>

<223> Primer

<400> 46

tcgagactga ctctcagccc accccgcagt agctc

35

<210> 47

<211> 50

<212> DNA

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<223> Primer

<400> 47

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<211> 30

<212> DNA

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<223> Primer

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<210> 49

<211> 31

<212> DNA

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<400> 49

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<210> 50

<211> 33

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<211> 30	
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gaacgtctca cgccaggcat cgatgccgat	30
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gaacgtctca ttgttagaga gggcgaagtc aaag	34
<210> 61	
<211> 36	
<212> DNA	
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<210> 62	
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ggaatctggt gggacacgat agcccagaag atacccgact gggcaagcgc cgggatttcg	120
gcgatatgga tccctccgc gagcaagggt atgagcggcg gctattcgat gggctacgac	180
ccctacgatt attttgcctt cggtgagta taccagaagg gaacqgtgga aacqaggttc	240
ggctcaaaggc aggagctcat aaacatgata aacaccgccc acgcctatgg catgaaggt	300

ata	gcccata	tagtcatcaa	ccaccgcgccc	ggcggtgacc	tggagtggaa	cccctcg	360
aac	gactata	cctggaccga	cttctcaaag	gtcgctcg	gtaaatacac	ggccaactac	420
ctc	gacttcc	acccgaacga	gctccatcg	ggcgattcc	gaacatttg	aggctatccc	480
gac	atgc	atgc	acgacaagag	ctgggaccag	tactggct	ggccagcca	540
gcg	catatc	tcaggagcat	cgcatcgat	gcctggcg	tgcactacgt	caaggcg	600
gtc	cccttgg	tcgtcaagga	ctggctgaac	tggtggggag	gctggcg	tggagagtac	660
tg	gacacca	acgtcgacgc	tgttctcaac	tgggcatact	cgagcggtgc	caaggcttt	720
gac	tgc	tctactaca	gatggacgag	gcctcgata	acaacaacat	tcccggcc	780
gtg	gacccc	tcagatacgg	tcagacagt	gtcagccgc	accgcgttcaa	ggctgtgac	840
ttt	gttagcca	accacgatac	cgacataatc	tggacaagt	atccagccta	cgcgttcatc	900
ctc	acctacg	agggccagcc	gacaatattc	taccgcgact	acgaggagtg	gctcaacaag	960
gata	agactca	agaacccat	ctggatacat	gacaacctcg	ccggagggag	cactgacatc	1020
gtt	tactacg	acaacgacga	gtgatattc	gtgagaaaacg	gctacggaa	caagccgg	1080
ctg	ataacat	acatcaac	ctgc	aaagccggaa	ggtgggtt	cgttccgaag	1140
ttc	gcaggct	cg	tgcataca	cgatcacc	gcaatctcg	gcccgtgg	1200
gtg	gactcaa	gcggctgg	ctac	ctcgag	gctcctgccc	acgaccggc	1260
tac	ggctact	ccgt	ctggag	ctactcg	gttgggtga	caacggcc	1299

&lt;210&gt; 67

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Environmental

&lt;400&gt; 67

Met	Ala	Leu	Glu	Glu	Gly	Ley	Ile	Met	Gln	Ala	Phe	Tyr	Trp	Asp	
1						5			10				15		
Val	Pro	Met	Gly	Gly	Ile	Trp	Trp	Asp	Thr	Ile	Gln	Lys	Ile	Pro	
						20			25				30		
Asp	Trp	Ala	Ser	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Pro	Pro	Ala	Ser
						35			40				45		
Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly	Tyr	Asp	Pro	Tyr	Asp	Tyr
						50			55				60		
Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val	Glu	Thr	Arg	Phe
						65			70				75		80
Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr	Ala	His	Ala	Tyr
						85			90				95		
Gly	Met	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg	Ala	Gly	Gly
						100			105				110		
Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Asn	Asp	Tyr	Thr	Trp	Thr	Asp	Phe
						115			120				125		
Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr	Leu	Asp	Phe	His
						130			135				140		
Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly	Thr	Phe	Gly	Tyr	Pro	
						145			150				155		160
Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln	Tyr	Trp	Leu	Trp	Ala	Ser
						165			170				175		
Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly	Ile	Asp	Ala	Trp
						180			185				190		
Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Ala	Pro	Trp	Val	Val	Lys	Asp	Trp
						195			200				205		
Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr	Trp	Asp	Thr	Asn
						210			215				220		
Val	Asp	Ala	Val	Leu	Asn	Trp	Ala	Tyr	Ser	Ser	Gly	Ala	Lys	Val	Phe
						225			230				235		240
Asp	Phe	Ala	Leu	Tyr	Tyr	Lys	Met	Asp	Glu	Ala	Phe	Asp	Asn	Asn	
						245			250				255		
Ile	Pro	Ala	Leu	Val	Asp	Ala	Leu	Arg	Tyr	Gly	Gln	Thr	Val	Val	Ser

260	265	270
Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp		
275	280	285
Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu		
290	295	300
Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys		
305	310	315
Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu Ala Gly Gly		
325	330	335
Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Val Arg		
340	345	350
Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Ala		
355	360	365
Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ser		
370	375	380
Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Trp		
385	390	395
Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala His Asp Pro		
405	410	415
Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly		
420	425	430

&lt;210&gt; 68

&lt;211&gt; 1386

&lt;212&gt; DNA

&lt;213&gt; Bacteria

&lt;400&gt; 68

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&lt;211&gt; 461

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   20              25              30  
 Glu Glu Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Ser  
   35              40              45  
 Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln Lys Ile Pro Glu Trp Tyr  
   50              55              60  
 Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met  
   65              70              75              80  
 Gly Gly Ala Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu  
   85              90              95  
 Gly Glu Tyr Asp Gln Lys Gly Thr Val Glu Thr Arg Phe Gly Ser Lys  
  100             105             110  
 Gln Glu Leu Val Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys  
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 Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Asp Leu Glu  
  130             135             140  
 Trp Asn Pro Phe Val Asn Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val  
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 Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu  
  165             170             175  
 Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala  
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 His Glu Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser Asn Glu Ser  
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 Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp  
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 Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala  
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 Leu Val Glu Ala Leu Lys Asn Gly Gly Thr Val Val Ser Arg Asp Pro  
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 Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp  
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 Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu  
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 Lys Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Asp  
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 Ile Val Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Val Arg Asn Gly Tyr  
  370             375             380  
 Gly Asp Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys  
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 Ala Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His  
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 Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Trp Val Asp Ser  
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 Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala His Asp Pro Ala Asn Gly

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Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly  
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